

Figure 1

GAGGTCCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGTCCTC	50
GGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTCAGCAGCTATGCTA	100
TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG	150
ATCATCCCTATCTTGGTACAGCAAACCTACGCACAGAAGTTCCAGGGCAG	200
AGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACATGGAGCTGA	250
GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCCA	300
TTACGATTTTGGAGTGGTCCACCCAAGACCACACTACTACTACTACAT	350
GGACGTCTGGGCAAAGGGACCACGGTACCGTCTCAAGC	390

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Figure 2

EVQLVQSGAEVKPGSSVKVSCKASGGTFSSYAI	50
<u>IIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARAP</u>	100
<u>LRFLEWSTQDHYYYYYMDVWGKTTTVSS</u>	130

Figure 3

ATGGGATGGTCATGTATCATCCTTTCTAGTAGCAACTGCAACTGGAGT	50
ACATTCAAGAGGTCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTG	100
GGTCCTCGGTGAAGGTCTCCTGCAAGGCTCTGGAGGCACCTTCAGCAGC	150
TATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGAT	200
GGGAGGGATCATCCCTATCTTGGTACAGCAAACATCGCACAGAAGTTCC	250
AGGGCAGAGTCACGATTACCGCGAACAAATCCACGAGCACAGCCTACATG	300
GAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATTACTGTGCGAG	350
AGCGCCATTACGATTTGGAGTGGTCCACCCAAGACCCTACTACTACT	400
ACTACATGGACGTCTGGGGCAAAGGGACCACGGTCACCGTCTCAAGCGCC	450
TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCAC	500
CTCTGGGGGACAGCGGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCG	550
AACCGGTGACGGTGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC	600
ACCTTCCC GGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT	650
GGTGACCGTGCCCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACG	700
TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCAAA	750
TCTTGTGACAAAACTCACACATGCCACCGTGCCAGCACCTGAACCTCCT	800
GGGGGGACCGTCAGTCTCCTCTTCCCCAAAACCCAAGGACACCCCTCA	850
TGATCTCCGGACCCCTGAGGTACATGCGTGGTGGGACGTGAGCCAC	900
GAAGACCCCTGAGGTCAAGTTCAACTGGTACGGACGGCGTGGAGGTGCA	950
TAATGCCAAGACAAAGCCGGGGAGGAGCAGTACAACAGCACGTACCGGG	1000
TGGTCAGCGTCCTCACCGCTGCACCAGGACTGGCTGAATGGCAAGGAG	1050
TACAAGTGCAGGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAAC	1100
CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGTACACCCCTGC	1150
CCCCATCCC GGAGGAGATGACCAAGAACCCAGGTCAAGCCTGACCTGCCTG	1200
GTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGTGGAGAGCAATGG	1250
GCAGCCGGAGAACAAACTACAAGACCAAGCAGCCTCCGTGCTGGACTCCGACG	1300
GCTCCTTCTCCTACAGCAAGCTCACCGTGGACAAGAGAGCAGGTGGCAG	1350
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCA	1400
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA	1440

Figure 4

MGWSCIILFLVATATGVHSEVQLVQSGAEVKPGSSVKVSCKASGGTFSS	50
YAI SWVRQAPGQGLEWMGGIPIPIFGTANYAQKFQGRVTITADKSTSTAYM	100
ELSSLRSEDTAVYYCARAPLRFLEWSTQDHYYYYYMDVWGKGTTVTVSSA	150
STKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVH	200
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK	250
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH	300
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE	350
YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL	400
VKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ	450
QGNVFSCSVMHEALHNHYTQKSLSLSPGK	479

Figure 5

TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGACAGAC	50
AGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGCAAGCT	100
GGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTATCTATGGTAAA	150
AAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCAGCTCAGG	200
AAACACAGCTTCCTTGACCATCACTGGGCTCAGGCGGAAGATGAGGCTG	250
ACTATTACTGTAACTCCGGGACAACAGTGATAACCGTCTGATATTGGC	300
GGCGGGACCAAGCTGACCGTCCTCAGT	327

Figure 6

SSELTQDPAVSVALGQTVRITC <u>QGDSLRSYYASWYQQKPGQAPVLVIYGK</u>	50
<u>NNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDNSDNRLIFG</u>	100
GGTKLTVLS	109

Figure 7

ATGGGATGGTCATGTATCATCCTTTCTAGTAGCAACTGCAACTGGAGT	50
<u>ACATT</u> CATCTTCTGAGCTGACTCAGGACCTGCTGTCTGTGGCCTTGG	100
GACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTAT	150
GCAAGCTGGTACCCAGCAGAAGCCAGGACAGGCCCTGTACTTGTATCTA	200
TGGTAAAAACAAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA	250
GCTCAGGAAACACAGCTTCTTGACCATCACTGGGCTCAGGCAGGAAGAT	300
GAGGCTGACTATTACTGTAACTCCCGGGACAACAGTGATAACCGTCTGAT	350
ATTGGCGGCGGGACCAAGCTGACCGTCCTCAGTCAGCCCCAAGGCTGCC	400
CCTCGGTCACTCTGTTCCGCCCTCCTGAGGAGCTTCAAGCCAACAAG	450
GCCACACTGGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGT	500
GGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCAGGAGTGGAGACACCA	550
CACCCCTCCAAACAAAGCAACAACAAGTACGGCCAGCAGCTATCTGAGC	600
CTGACGCCCTGAGCAGTGGAAAGTCCCACAGAAAGCTACAGCTGCCAGGTAC	650
GCATGAAGGGAGCACCGTGGAGAAGACAGTGCCCTGCAGAATGCTCTT	700
GA	702

Figure 8

MGWSCI ILFLVATATGVHSSSEL TQDPAVSVALGQTVRITCQGDSLRSYY	50
<u>ASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAED</u>	100
EADYYCNSRDNSDNRLIFGGGTKLTVLSQPKAAPSVTLFPPSSEELQANK	150
ATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLS	200
<i>LTPEQWKSHRSYSCQVTHEGSTVEKTVAPAECs</i>	233

Figure 9

TCTTCTGAGCTGACTCAGGACCCCTGCTGTGTCTGTGGCCTGGGACAGAC	50
AGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGCAACCT	100
GGTACCAGCAGAAGCCAGGACAGGCCCTATTCTTGTCACTATGGTGAA	150
AATAAGCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCAGCTCAGG	200
AAACACAGCTTCCTTGACCATCACTGGGCTCAGGCAGAAGATGAGGCTG	250
ACTACTATTGTAATCTCGGGATGGCAGTGGTCAACATCTGGTGGTTCGGC	300
GGAGGGACCAAGCTGACCGTCCTAGGT	327

Figure 10

SSELTDPAVSVALGQTVRITCQGDSLRSYYATWYQQKPGQAPILVYGE	50
NKRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCKSRDGSGQHLVFG	100
GGTKLTVLG	109

Figure 11

ATGGGATGGTCATGTATCATCCTTTCTAGTAGCAACTGCAACTGGAGT	50
ACATTCATCTTCTGAGCTGACTCAGGACCTGCTGTGTCTGGCCTTGG	100
GACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTAT	150
GCAACCTGGTACCAGCAGAAGCCAGGACAGGCCCTATTCTGTCTGGCTCCA	200
TGGTGAAAATAAGCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA	250
GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGCTCAGGCAGAAGAT	300
GAGGCTGACTACTATTGTAAATCTCGGGATGGCAGTGGTCAACATCTGGT	350
GTTCGGCGGAGGGACCAAGCTGACCGTCTAGGTCAAGCCAAAGGCTGCC	400
CCTCGGTCACTCTGTTCCGCCCTCTGAGGAGCTCAAGCCAACAAG	450
GCCACACTGGTGTCTATAAGTGACTTCTACCCGGAGCCGTGACAGT	500
GGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA	550
CACCCCTCCAAACAAAGCAACAACAAGTACCGGGCCAGCAGCTATCTGAGC	600
CTGACGCCCTGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCAGGTAC	650
GCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCTGCAGAATGCTCTT	700
GA	702

Figure 12

<u>MGWSCIILFLVATATGVHSS</u> ELTQDPAVSVALGQTVRITCQGDSLRSYY	50
ATWYQQKPGQAPILVIYGENKRPSGIPDRFSGSSSGNTASLTITGAQAED	100
EADYYCKSRDGSGQHLVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANK	150
ATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSYLS	200
LTPEQWKSHRSYSCQVTHEGSTVEKTVAPAECs	233

Figure 13

Heavy chain			
CDR1	CDR2	CDR3	
SYAIS	GIIPIFGTANYAQKFQG	APLRFLEWSTQDHYYYYYMDV	2F8/A12
Light chain			
CDR1	CDR2	CDR3	
QGDSLRSYYAS	GKNNRPS	NSRDNSDNRLI	2F8
QGDSLRSYYAT	GENKRPS	KSRDGSGQHLV	A12

Figure 14

CDR1

CDR2

CDR3

2F8 10 20 30 40 50

A12 S S E L T Q D P A V S V A L G Q T V R I T C Q G D S L R S Y Y A S W Y Q Q K P G Q A P V L V I Y G K

A12 S S E L T Q D P A V S V A L G Q T V R I T C Q G D S L R S Y Y A T W Y Q Q K P G Q A P I L V I Y G E

2F8 60 70 80 90 100

A12 N K R P S G I P D R F S G S S S G N T A S L T I T G A Q A E D E A D Y Y C N S R D N S D N R L I F G

A12 N K R P S G I P D R F S G S S S G N T A S L T I T G A Q A E D E A D Y Y C K S R D G S G Q H L V F G

2F8 109

A12 G G T K L T V L S

A12 G G T K L T V L G

Figure 15

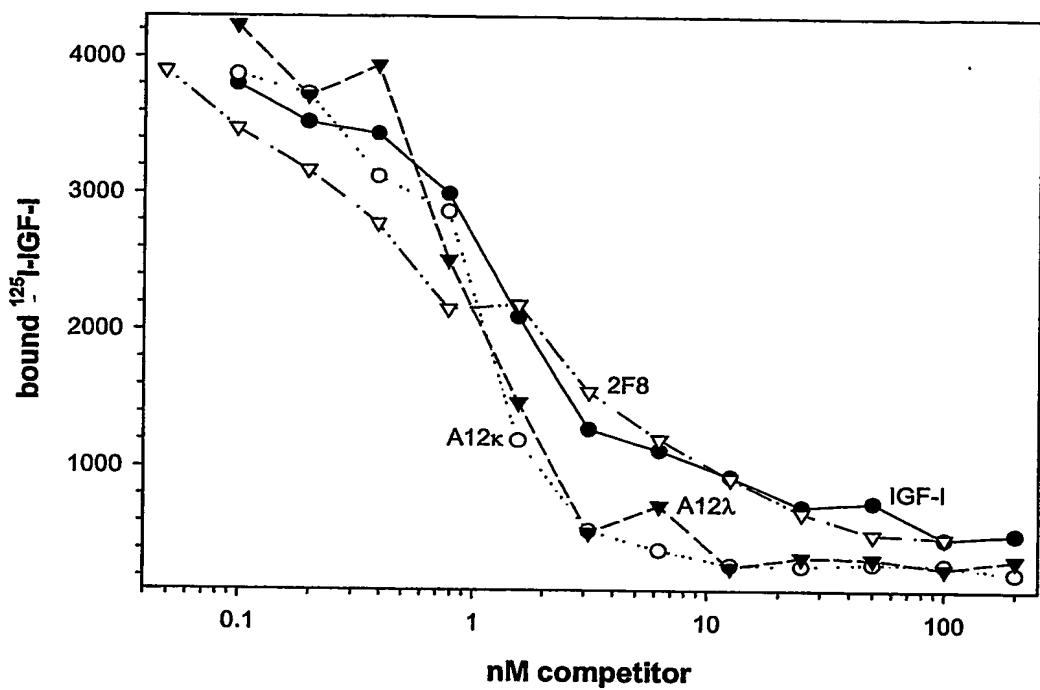


Figure 16

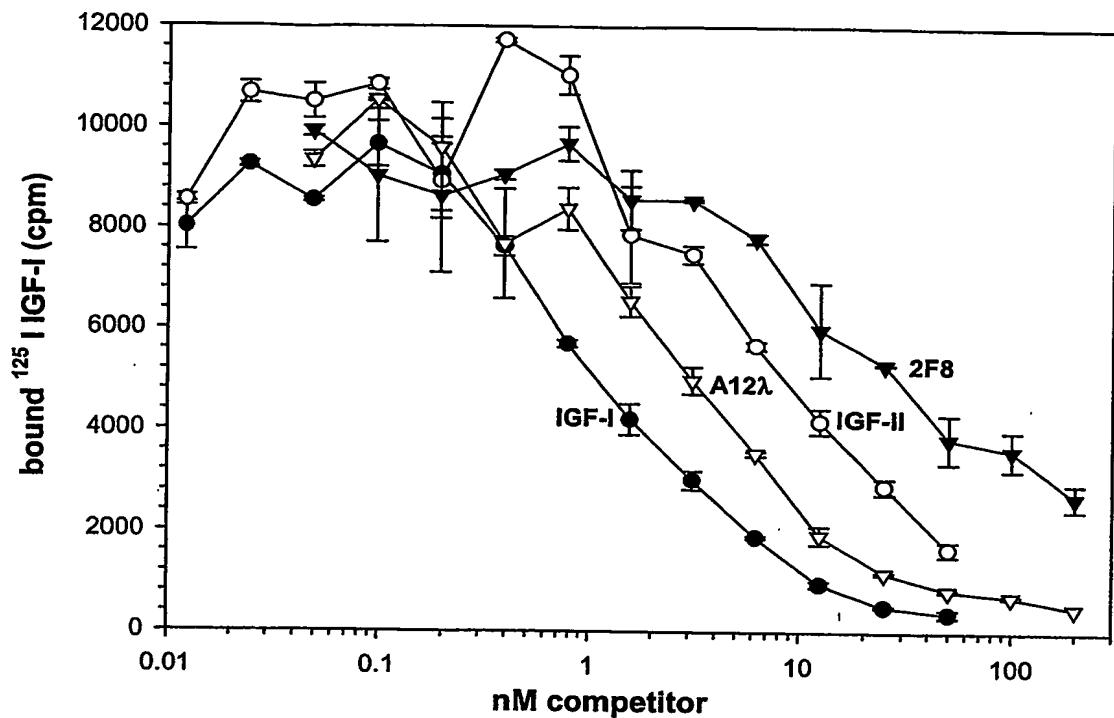


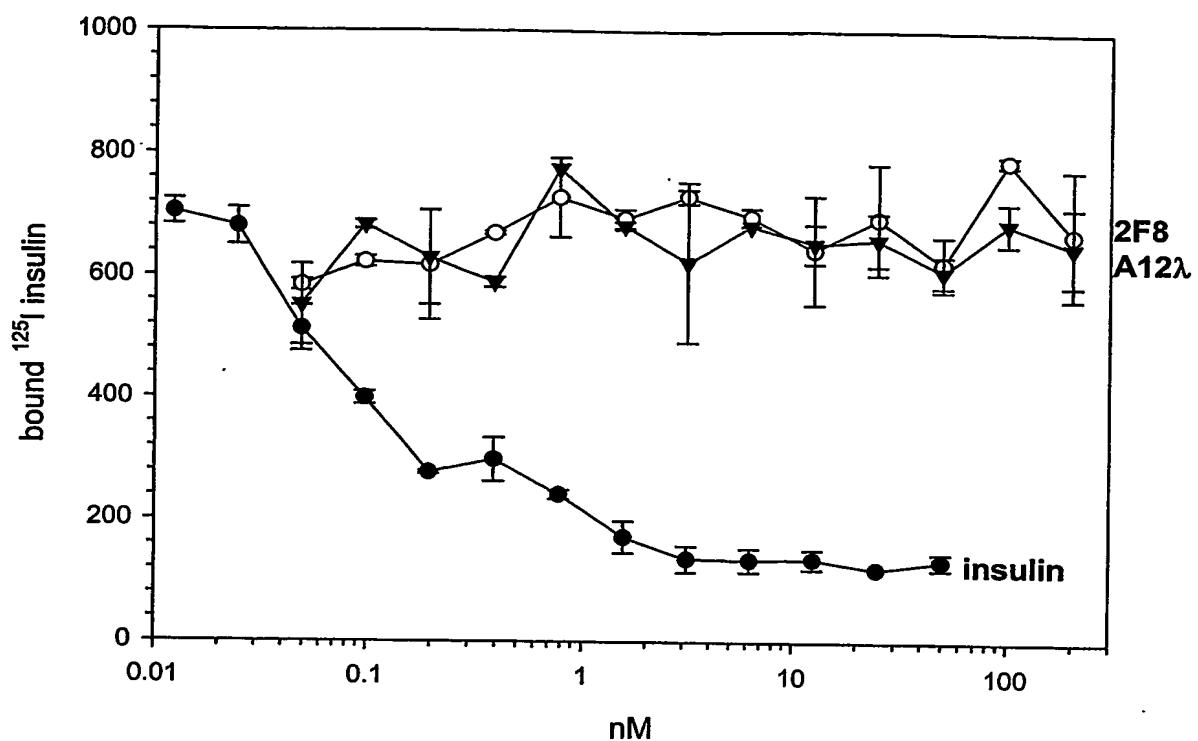
Figure 17

Figure 18A

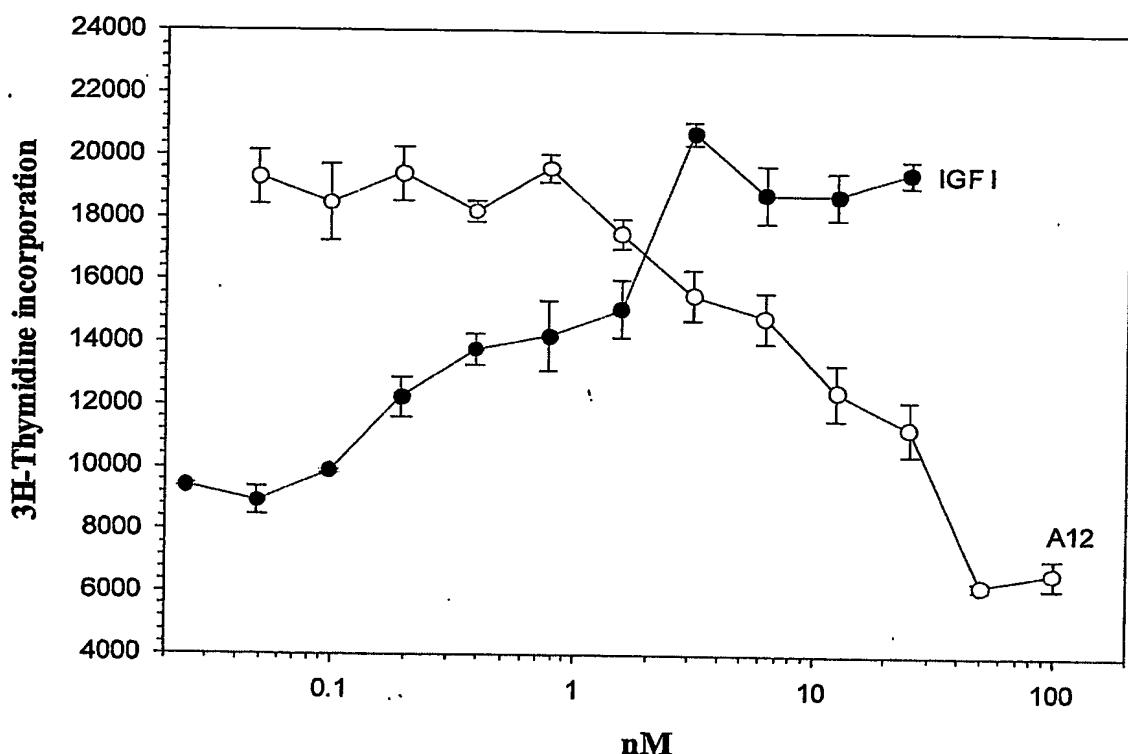


Figure 18B

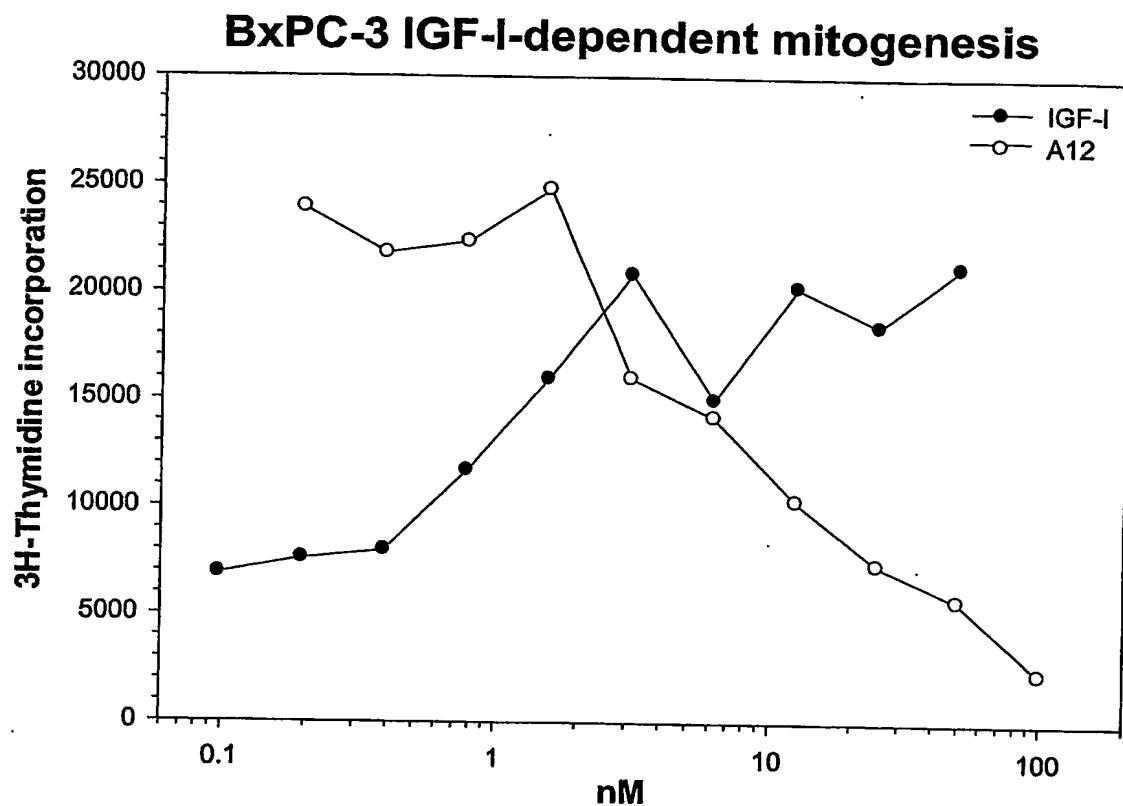


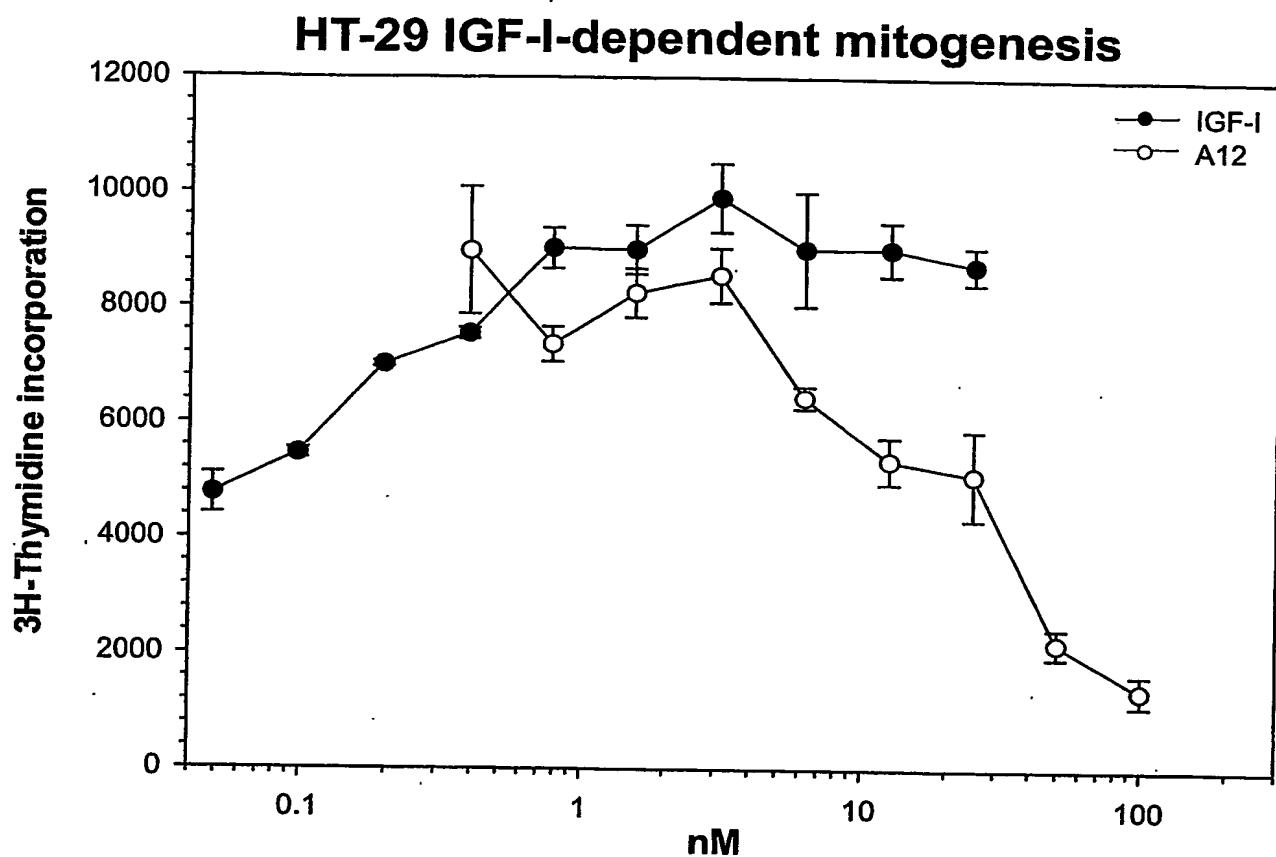
Figure 18C

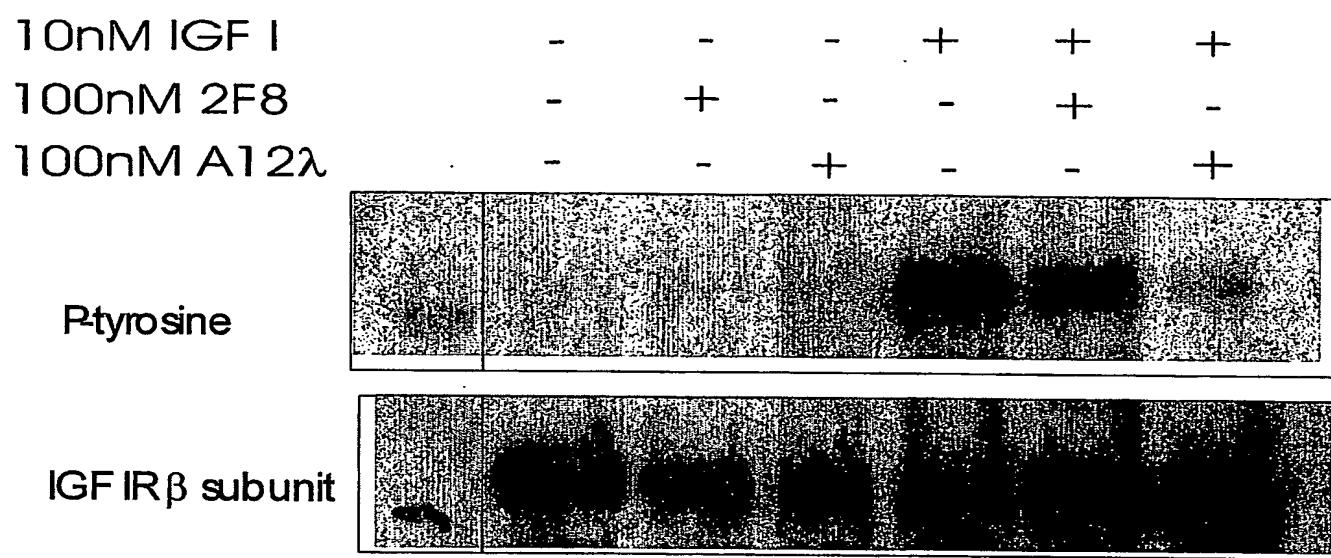
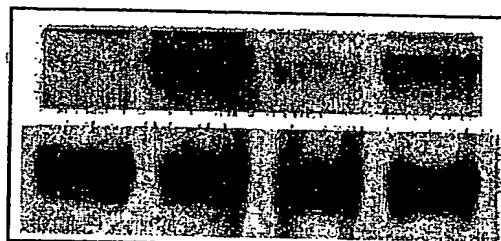
Figure 19A

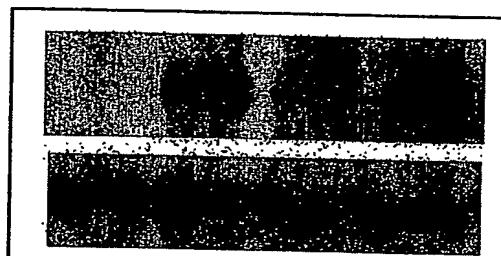
Figure 19B**IGF-I-dependent IGF-I receptor phosphorylation**

10nM IGF I	-	+	+	+
100nM A12	-	-	+	-
Control	-	-	-	+

HT-29

P-tyrosine

IGF IR β subunit

BXPC3

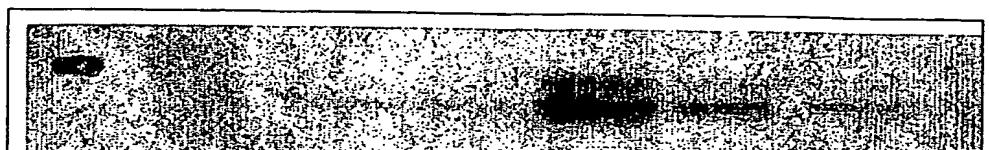
P-tyrosine

IGF IR β subunit

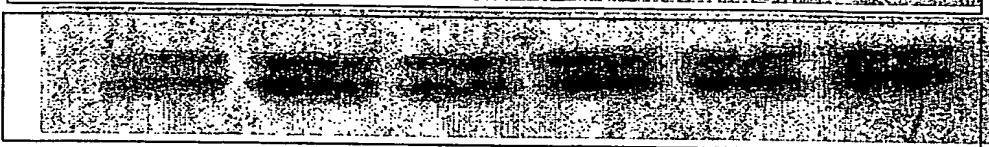
Figure 20A

10nM IGF I	-	-	-	+	+	+
100nM 2F8	-	+	-	-	+	-
100nM A12 λ	-	-	+	-	-	+

P-MAPK



MAPK

Antibody concentration: 100nM 50nM 10nM

10nM IGF I	-	-	-	+	+	+	+	+	+	+
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Mab - 2F8	-	-	-	-	+	-	+	-	+	-
------------------	---	---	---	---	---	---	---	---	---	---

Mab - A12λ	-	-	-	-	-	+	-	+	-	+
--------------------------------------	---	---	---	---	---	---	---	---	---	---

P-AKT



Figure 20B

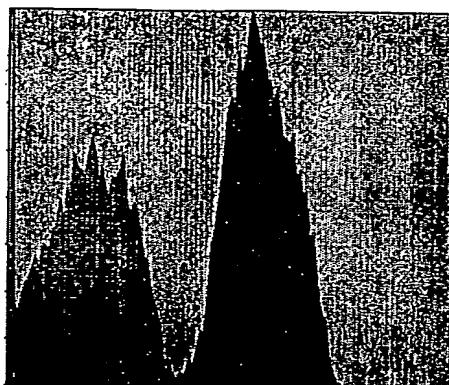
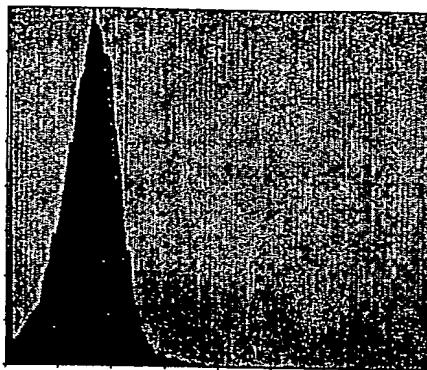
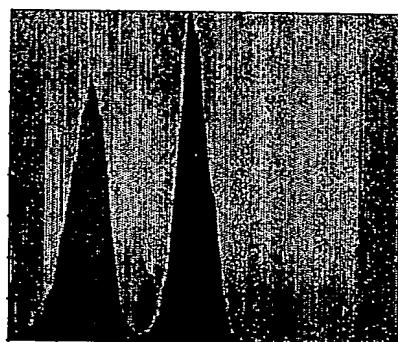
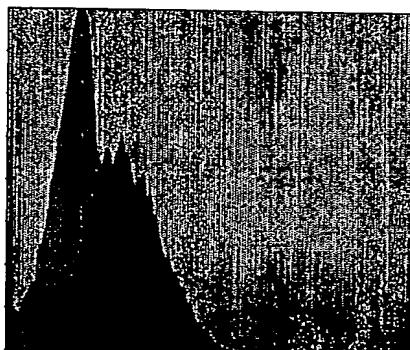
Figure 21**MCF 7****MF= 100****R****MF= 0.5****HE****MF= 30****Lewis Lung****MF= 13**

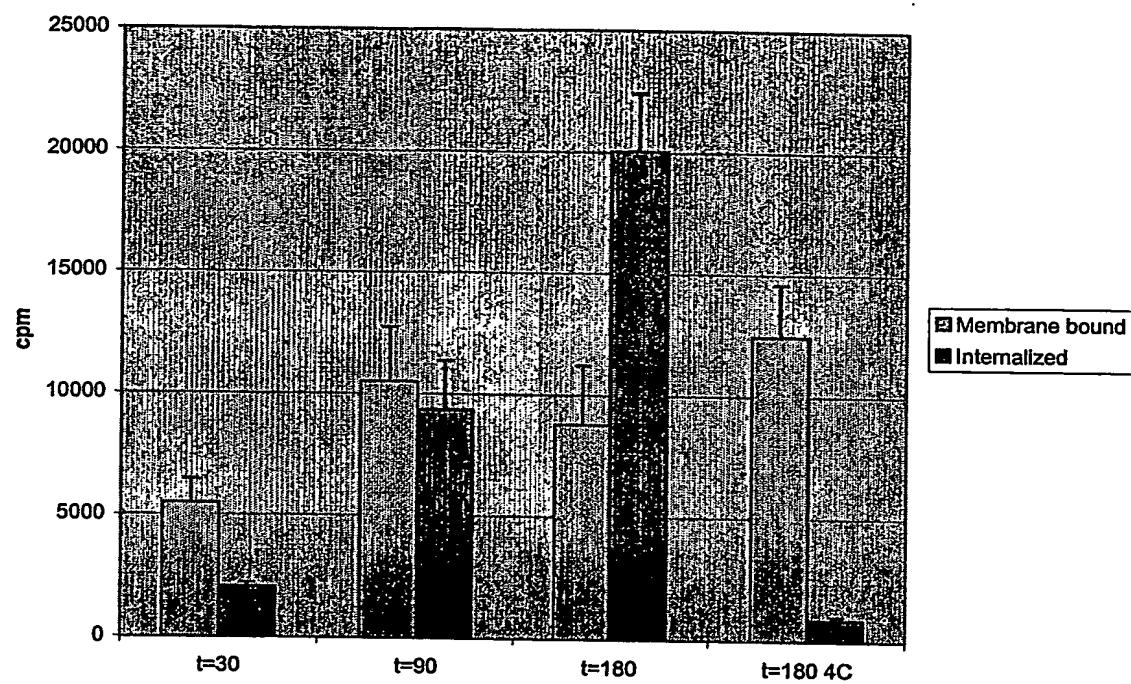
Figure 22A

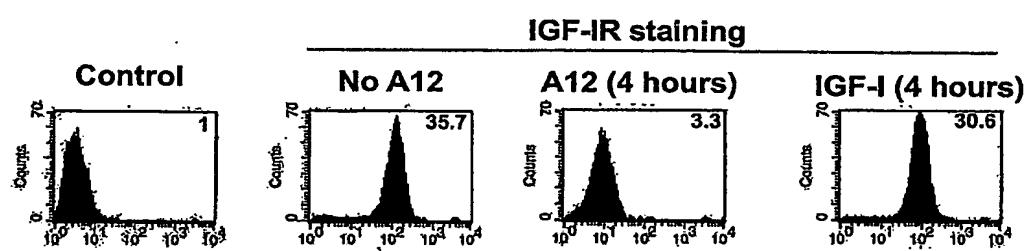
Figure 22B

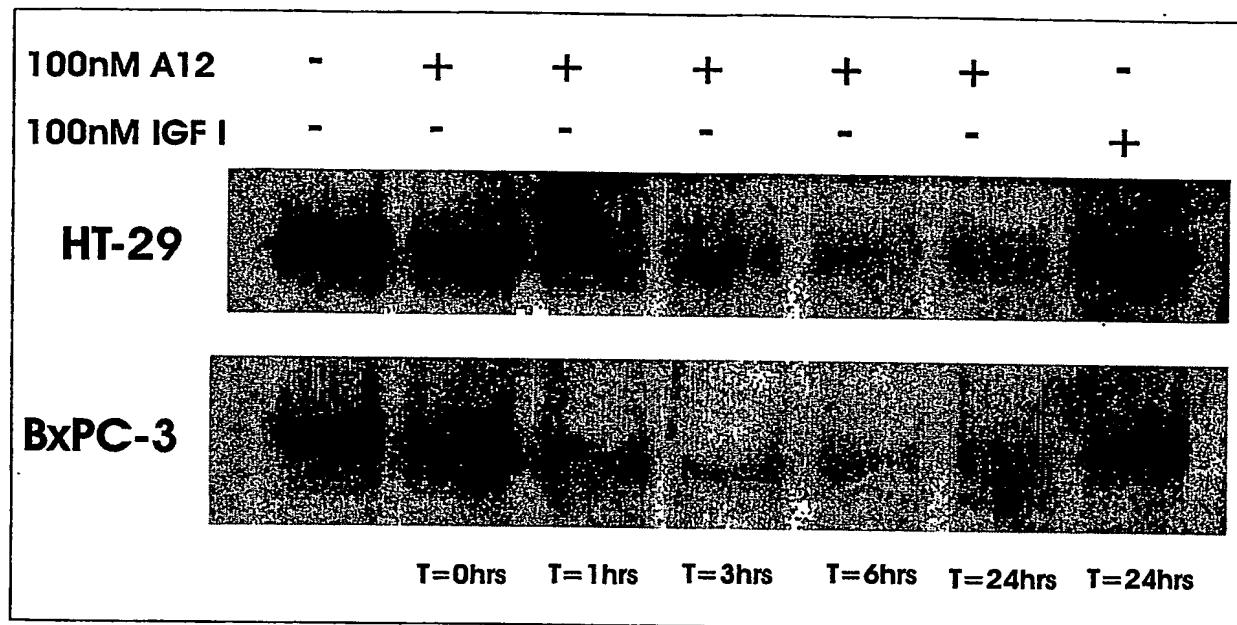
Figure 22C**Antibody-mediated IGF-I receptor degradation**

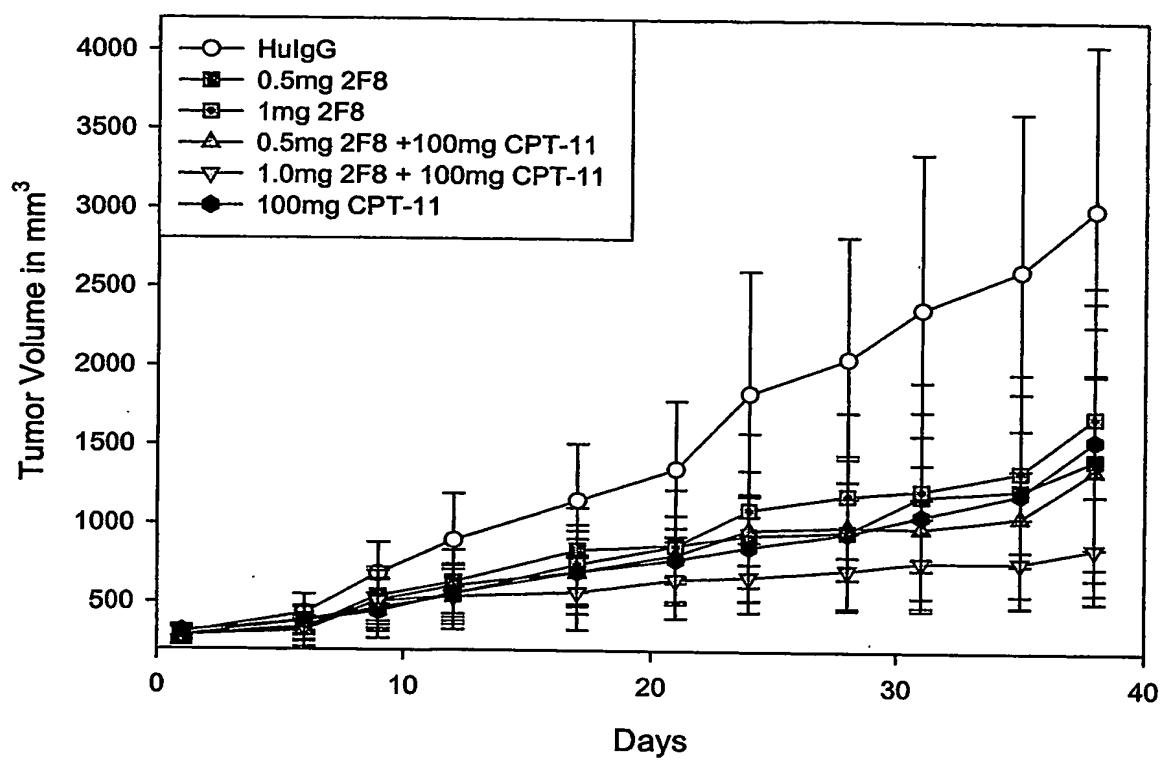
Figure 23

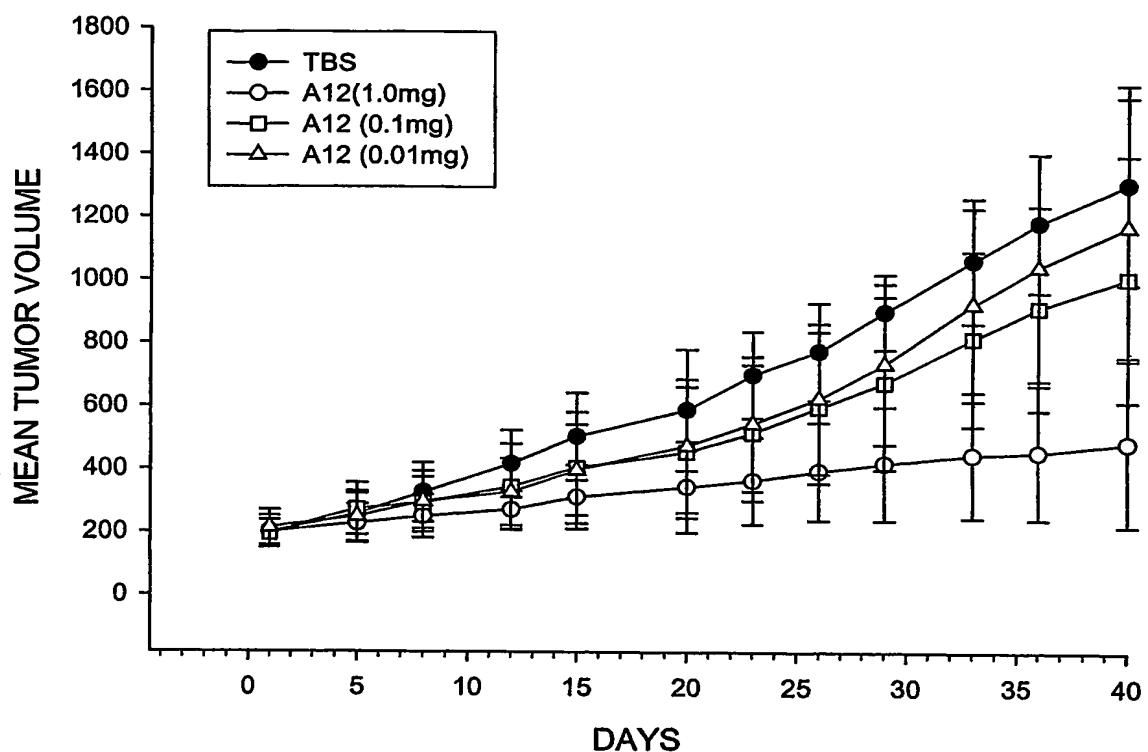
Figure 24

Figure 25:

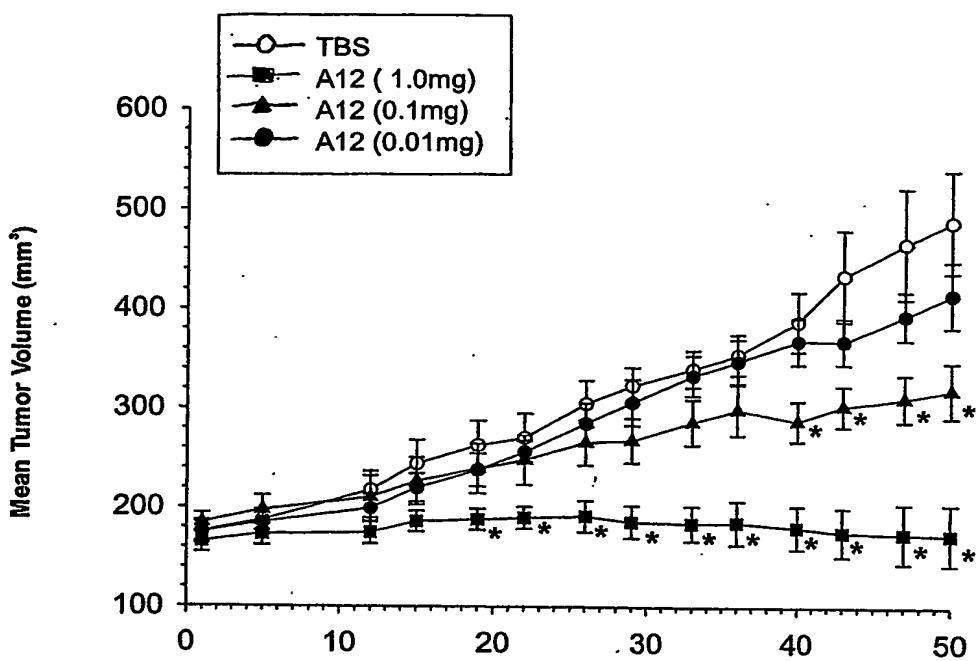


Figure 26

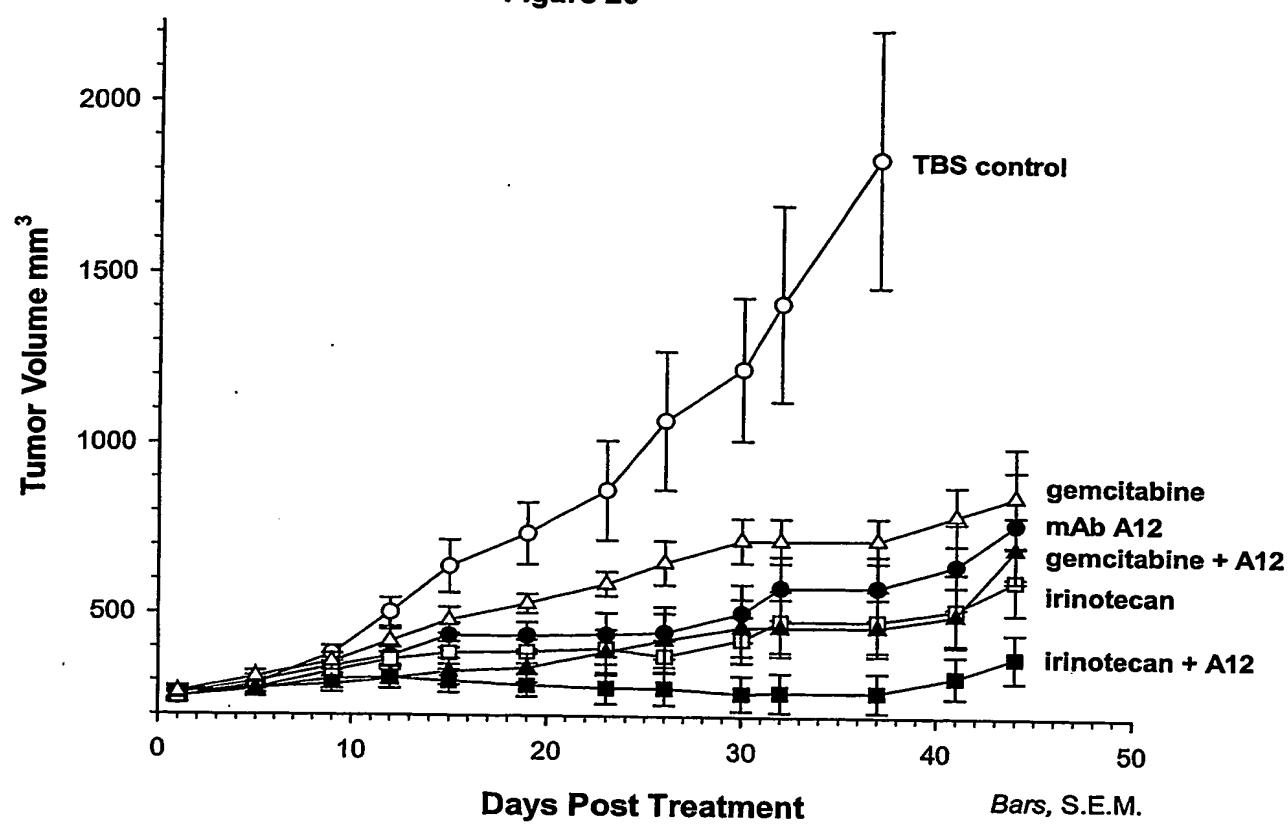
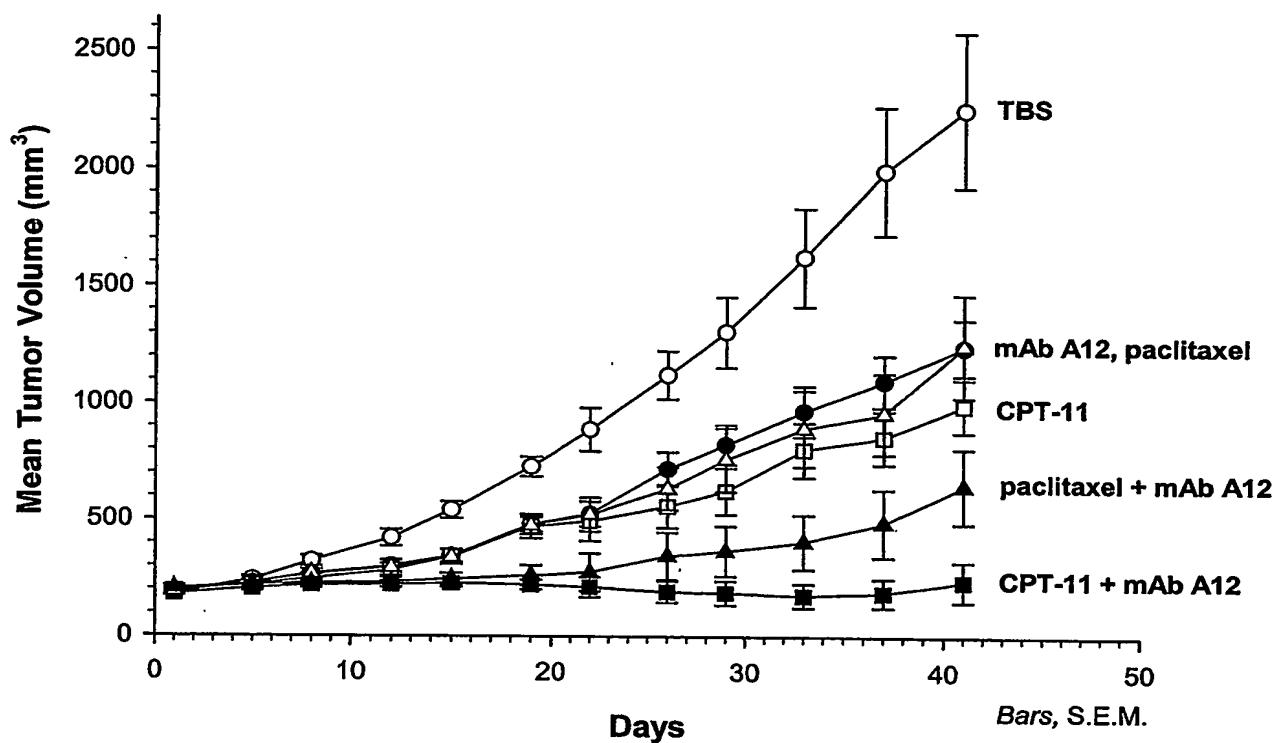


Figure 27



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